Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/057,843C

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ____ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ____ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ____ Variable Length

Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0 "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) ____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 ____ Skipped Sequences (OLD RULES)

Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ____ Skipped Sequences (NEW RULES)

Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ____ Use of n's or Xaa's (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.

10 ____ Invalid <213> Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial-Sequence

11 ____ Use of <220>

Sequence(s) 1-2 (maybe more) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0 "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

RECEIVED

JUN 0 7 2002

TECH CENTER 1600/2900

1600

Does Not Comply
Corrected Diskette Needed

```
      RAW SEQUENCE LISTING              DATE: 05/29/2002
      PATENT APPLICATION:  US/09/051,843C    TIME: 16:33:26

      Input Set : A:\11373.txt
      Output Set: N:\CRF3\05292002\I051843C.raw

 3 <110> APPLICANT: Willson, Tracy
 4        Nicola, Nicos A.
 5        Hilton, Douglas J.
 6        Metcalf, Donald
 7        Zhang, Jian G.
 9 <120> TITLE OF INVENTION: NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES
10        ENCODING SAME
12 <130> FILE REFERENCE: Davies cc
14 <140> CURRENT APPLICATION NUMBER: 09/051,843C
15 <141> CURRENT FILING DATE: 1998-06-29
17 <160> NUMBER OF SEQ ID NOS: 11
19 <170> SOFTWARE: PatentIn Ver. 2.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 1383
23 <212> TYPE: DNA
24 <213> ORGANISM: Unknown     see item 11 on Errn Summary Sheet
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (61)..(1338)
30 <220> FEATURE:
31 <221> NAME/KEY: unsure
32 <222> LOCATION: (121)
33 <223> OTHER INFORMATION: n=authors are unsure of exact sequence in this
34        region
36 <220> FEATURE:
37 <221> NAME/KEY: unsure
38 <222> LOCATION: (122)
39 <223> OTHER INFORMATION: n=authors are unsure of exact sequence in this
40        region
42 <220> FEATURE:
43 <221> NAME/KEY: unsure
44 <222> LOCATION: (123)
45 <223> OTHER INFORMATION: n=authors are unsure of exact sequence in this
46        region
48 <220> FEATURE:
49 <221> NAME/KEY: unsure
50 <222> LOCATION: (640)
51 <223> OTHER INFORMATION: n=authors are unsure of exact sequence in this
52        region
55 <220> FEATURE:
56 <221> NAME/KEY: unsure
57 <222> LOCATION: (641)
58 <223> OTHER INFORMATION: n=authors are unsure of exact sequence in this
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RAW SEQUENCE LISTING   DATE: 05/29/2002
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59       region
61 <220> FEATURE:
62 <221> NAME/KEY: unsure
63 <222> LOCATION: (642)
64 <223> OTHER INFORMATION: n=authors are unsure of exact sequence in this
65       region
67 <400> SEQUENCE: 1
68 tgaaaagata gaataaatgg cctcgtgccg aattcggcac gagccgaggc gagggcctgc 60
70 atg gcg cgg cca gcg ctg ctg ggc gag ctg ttg gtg ctg cta ctg tgg     108
71 Met Ala Arg Pro Ala Leu Leu Gly Glu Leu Leu Val Leu Leu Leu Trp
72  1               5                  10                  15
74 acc gcc acc gtg nnn ggc caa gtt gcc gcg gcc aca gaa gtt cag cca     156
75 Thr Ala Thr Val Xaa Gly Gln Val Ala Ala Ala Thr Glu Val Gln Pro
76              20                  25                  30
78 cct gtg acg aat ttg agc gtc tct gtc gaa aat ctc tgc acg ata ata     204
79 Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Ile Ile
80          35                  40                  45
82 tgg acg tgg agt cct cct gaa gga gcc agt cca aat tgc act ctc aga     252
83 Trp Thr Trp Ser Pro Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg
84      50                  55                  60
86 tat ttt agt cac ttt gat gac caa cag gat aag aaa att gct cca gaa     300
87 Tyr Phe Ser His Phe Asp Asp Gln Gln Asp Lys Lys Ile Ala Pro Glu
88 65                  70                  75                  80
90 act cat cgt aaa gag gaa tta ccc ctg gat gag aaa atc tgt ctg cag     348
91 Thr His Arg Lys Glu Glu Leu Pro Leu Asp Glu Lys Ile Cys Leu Gln
92              85                  90                  95
94 gtg ggc tct cag tgt agt gcc aat gaa agt gag aag cct agc cct ttg     396
95 Val Gly Ser Gln Cys Ser Ala Asn Glu Ser Glu Lys Pro Ser Pro Leu
96              100                 105                 110
98 gtg aaa aag tgc atc tca ccc cct gaa ggt gat cct gag tcc gct gtg     444
99 Val Lys Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val
100          115                 120                 125
102 act gag ctc aag tgc att tgg cat aac ctg agc tat atg aag tgt tcc    492
103 Thr Glu Leu Lys Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser
104      130                 135                 140
106 tgg ctc cct gga agg aat aca agc cct gac aca cac tat act ctg tac    540
107 Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr His Tyr Thr Leu Tyr
108 145                 150                 155                 160
110 tat tgg tac agc agc ctg gag aaa agt cgt caa tgt gaa aac atc tat    588
111 Tyr Trp Tyr Ser Ser Leu Glu Lys Ser Arg Gln Cys Glu Asn Ile Tyr
112                  165                 170                 175
114 aga gaa ggt caa cac att gct tgt tcc ttt aaa ttg act aaa gtg gaa    636
115 Arg Glu Gly Gln His Ile Ala Cys Ser Phe Lys Leu Thr Lys Val Glu
116                  180                 185                 190
118 cct nnn agt ttt gaa cat cag aac gtt caa ata atg gtc aag gat aat    684
119 Pro Xaa Ser Phe Glu His Gln Asn Val Gln Ile Met Val Lys Asp Asn
120          195                 200                 205
122 gct ggg aaa att agg cca tcc tgc aaa ata gtg tct tta act tcc tat    732
123 Ala Gly Lys Ile Arg Pro Ser Cys Lys Ile Val Ser Leu Thr Ser Tyr
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RAW SEQUENCE LISTING   DATE: 05/29/2002
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Input Set : A:\11373.txt
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124      210                    215                    220
126 gtg aaa cct gat cct cca cat att aaa cat ctt ctc ctc aaa aat ggt    780
127 Val Lys Pro Asp Pro Pro His Ile Lys His Leu Leu Leu Lys Asn Gly
128 225                    230                    235                    240
130 gcc tta tta gtg cag tgg aag aat cca caa aat ttt aga agc aga tgc    828
131 Ala Leu Leu Val Gln Trp Lys Asn Pro Gln Asn Phe Arg Ser Arg Cys
132                    245                    250                    255
134 tta act tat gaa gtg gag gtc aat aat act caa acc gac cga cat aat    876
135 Leu Thr Tyr Glu Val Glu Val Asn Asn Thr Gln Thr Asp Arg His Asn
136                260                    265                    270
138 att tta gag gtt gaa gag gac aaa tgc cag aat tcc gaa tct gat aga    924
139 Ile Leu Glu Val Glu Glu Asp Lys Cys Gln Asn Ser Glu Ser Asp Arg
140            275                    280                    285
142 aac atg gag ggt aca agt tgt ttc caa ctc cct ggt gtt ctt gcc gac    972
143 Asn Met Glu Gly Thr Ser Cys Phe Gln Leu Pro Gly Val Leu Ala Asp
144      290                    295                    300
146 gct gtc tac aca gtc aga gta aga gtc aaa aca aac aag tta tgc ttt   1020
147 Ala Val Tyr Thr Val Arg Val Arg Val Lys Thr Asn Lys Leu Cys Phe
148 305                    310                    315                    320
150 gat gac aac aaa ctg tgg agt gat tgg agt gaa gca cag agt ata ggt   1068
151 Asp Asp Asn Lys Leu Trp Ser Asp Trp Ser Glu Ala Gln Ser Ile Gly
152                    325                    330                    335
154 aag gag caa aac tcc acc ttc tac acc acc atg tta ctc acc att cca   1116
155 Lys Glu Gln Asn Ser Thr Phe Tyr Thr Thr Met Leu Leu Thr Ile Pro
156                340                    345                    350
158 gtc ttt gtc gca gtg gca gtc ata atc ctc ctt ttt tac ctg aaa agg   1164
159 Val Phe Val Ala Val Ala Val Ile Ile Leu Leu Phe Tyr Leu Lys Arg
160            355                    360                    365
162 ctt aag atc att ata ttt cct cca att cct gat cct ggc aag att ttt   1212
163 Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe
164      370                    375                    380
166 aaa gaa atg ttt gga gac cag aat gat gat acc ctg cac tgg aag aag   1260
167 Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys
168 385                    390                    395                    400
170 tat gac atc tat gag aaa caa tcc aaa gaa gaa acg gat tct gta gtg   1308
171 Tyr Asp Ile Tyr Glu Lys Gln Ser Lys Glu Glu Thr Asp Ser Val Val
172                    405                    410                    415
174 ctg ata gaa aac ctg aag aaa gca gct cct tgatggggag aagtgatttc   1358
175 Leu Ile Glu Asn Leu Lys Lys Ala Ala Pro
176                420                    425
178 tttcttgcct tcaatgtgac cctgt                                       1383
181 <210> SEQ ID NO: 2
182 <211> LENGTH: 426
183 <212> TYPE: PRT
184 <213> ORGANISM: Unknown
186 <220> FEATURE:
187 <221> NAME/KEY: unsure
188 <222> LOCATION: (21)
189 <223> OTHER INFORMATION: authors are unsure about the sequence assignment
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see item 11

Please correct any subsequent sequences showing this error.

RAW SEQUENCE LISTING   DATE: 05/29/2002
PATENT APPLICATION: US/09/051,843C   TIME: 16:33:26

Input Set : A:\11373.txt
Output Set: N:\CRF3\05292002\I051843C.raw

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191 <220> FEATURE:
193 <221> NAME/KEY: unsure
194 <222> LOCATION: (194)
195 <223> OTHER INFORMATION: authors are unsure about the sequence assignment
197 <400> SEQUENCE: 2
198 Met Ala Arg Pro Ala Leu Leu Gly Glu Leu Leu Val Leu Leu Leu Trp
199  1               5                  10                  15
201 Thr Ala Thr Val Xaa Gly Gln Val Ala Ala Ala Thr Glu Val Gln Pro
202              20              25              30
204 Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Ile Ile
205              35              40              45
207 Trp Thr Trp Ser Pro Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg
208          50              55              60
210 Tyr Phe Ser His Phe Asp Asp Gln Gln Asp Lys Lys Ile Ala Pro Glu
211  65              70                  75                      80
213 Thr His Arg Lys Glu Glu Leu Pro Leu Asp Glu Lys Ile Cys Leu Gln
214              85              90                  95
216 Val Gly Ser Gln Cys Ser Ala Asn Glu Ser Glu Lys Pro Ser Pro Leu
217             100             105             110
219 Val Lys Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val
220          115             120             125
222 Thr Glu Leu Lys Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser
223         130             135             140
225 Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr His Tyr Thr Leu Tyr
226 145             150             155             160
228 Tyr Trp Tyr Ser Ser Leu Glu Lys Ser Arg Gln Cys Glu Asn Ile Tyr
229             165             170             175
231 Arg Glu Gly Gln His Ile Ala Cys Ser Phe Lys Leu Thr Lys Val Glu
232             180             185             190
234 Pro Xaa Ser Phe Glu His Gln Asn Val Gln Ile Met Val Lys Asp Asn
235         195             200             205
237 Ala Gly Lys Ile Arg Pro Ser Cys Lys Ile Val Ser Leu Thr Ser Tyr
238     210             215             220
240 Val Lys Pro Asp Pro Pro His Ile Lys His Leu Leu Leu Lys Asn Gly
241 225             230             235             240
243 Ala Leu Leu Val Gln Trp Lys Asn Pro Gln Asn Phe Arg Ser Arg Cys
244             245             250             255
246 Leu Thr Tyr Glu Val Glu Val Asn Asn Thr Gln Thr Asp Arg His Asn
247         260             265             270
249 Ile Leu Glu Val Glu Glu Asp Lys Cys Gln Asn Ser Glu Ser Asp Arg
250         275             280             285
252 Asn Met Glu Gly Thr Ser Cys Phe Gln Leu Pro Gly Val Leu Ala Asp
253     290             295             300
255 Ala Val Tyr Thr Val Arg Val Arg Val Lys Thr Asn Lys Leu Cys Phe
256 305             310             315             320
258 Asp Asp Asn Lys Leu Trp Ser Asp Trp Ser Glu Ala Gln Ser Ile Gly
259             325             330             335
262 Lys Glu Gln Asn Ser Thr Phe Tyr Thr Thr Met Leu Leu Thr Ile Pro
263             340             345             350
```

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PATENT APPLICATION: US/09/051,843C   TIME: 16:33:26

Input Set : A:\11373.txt
Output Set: N:\CRF3\05292002\I051843C.raw

```
265 Val Phe Val Ala Val Ala Val Ile Ile Leu Leu Phe Tyr Leu Lys Arg
266         355                 360                 365
268 Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe
269     370                 375                 380
271 Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys
272 385                 390                 395                 400
274 Tyr Asp Ile Tyr Glu Lys Gln Ser Lys Glu Glu Thr Asp Ser Val Val
275             405                 410                 415
277 Leu Ile Glu Asn Leu Lys Lys Ala Ala Pro
278         420                 425
281 <210> SEQ ID NO: 3
282 <211> LENGTH: 1383
283 <212> TYPE: DNA
284 <213> ORGANISM: Homo sapiens
286 <220> FEATURE:
287 <221> NAME/KEY: CDS
288 <222> LOCATION: (61)..(1338)
290 <400> SEQUENCE: 3
291 gagtctaaca cggaccaagg agtttaacac gtgcggccgg gttccgaggc gagaggctgc 60
293 atg gag tgg ccg gcg cgg ctc tgc ggg ctg tgg gcg ctg ctg ctc tgc    108
294 Met Glu Trp Pro Ala Arg Leu Cys Gly Leu Trp Ala Leu Leu Leu Cys
295   1               5                  10                  15
297 gcc ggc ggc ggg ggc ggg ggc ggg ggc gcg cct acg gaa act cag cca    156
298 Ala Gly Gly Gly Gly Gly Gly Gly Gly Ala Pro Thr Glu Thr Gln Pro
299             20                  25                  30
301 cct gtg aca aat ttg agt gtc tct gtt gaa aac ctc tgc aca gta ata    204
302 Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Val Ile
303             35                  40                  45
305 tgg aca tgg aat cca ccc gag gga gcc agc tca aat tgt agt cta tgg    252
306 Trp Thr Trp Asn Pro Pro Glu Gly Ala Ser Ser Asn Cys Ser Leu Trp
307         50                  55                  60
309 tat ttt agt cat ttt ggc gac aaa caa gat aag aaa ata gct ccg gaa    300
310 Tyr Phe Ser His Phe Gly Asp Lys Gln Asp Lys Lys Ile Ala Pro Glu
311 65                  70                  75                  80
313 act cgt cgt tca ata gaa gta ccc ctg aat gag agg att tgt ctg caa    348
314 Thr Arg Arg Ser Ile Glu Val Pro Leu Asn Glu Arg Ile Cys Leu Gln
315                 85                  90                  95
317 gtg ggg tcc cag tgt agc acc aat gag agt gag aag cct agc att ttg    396
318 Val Gly Ser Gln Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile Leu
319             100                 105                 110
321 gtt gaa aaa tgc atc tca ccc cca gaa ggt gat cct gag tct gct gtg    444
322 Val Glu Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val
323         115                 120                 125
325 act gag ctt caa tgc att tgg cac aac ctg agc tac atg aag tgt tct    492
326 Thr Glu Leu Gln Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser
327         130                 135                 140
329 tgg ctc cct gga agg aat acc agt ccc gac act aac tat act ctc tac    540
330 Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu Tyr
331 145                 150                 155                 160
```

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 05/29/2002
PATENT APPLICATION: US/09/051,843C   TIME: 16:33:27

Input Set : A:\11373.txt
Output Set: N:\CRF3\05292002\I051843C.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 121,122,123,640,641,642
Seq#:1; Xaa Pos. 21,194
Seq#:2; Xaa Pos. 21,194
Seq#:9; Xaa Pos. 3
Seq#:10; Xaa Pos. 24
Seq#:11; Xaa Pos. 24